

BINF 731

# Protein Structure Analysis

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# AlphaFold

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Article

## Highly accurate protein structure prediction with AlphaFold

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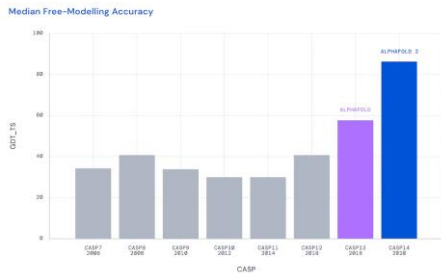
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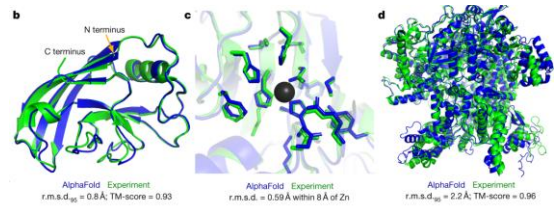
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Proteins are essential to life, and understanding their structure can facilitate a mechanistic understanding of their function. Through an enormous experimental effort<sup>1</sup>, the structures of around 100,000 unique proteins have been determined<sup>2</sup>, but this represents a small fraction of the billions of known protein sequences<sup>3</sup>. Structural coverage is bottlenecked by the months to years of painstaking effort required to determine a single protein structure. Accurate computational approaches are needed to address this gap and to enable large-scale structural bioinformatics. Predicting the three-dimensional structure that a protein will adopt based solely on its amino acid

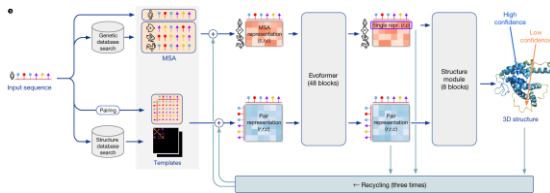
# AlphaFold



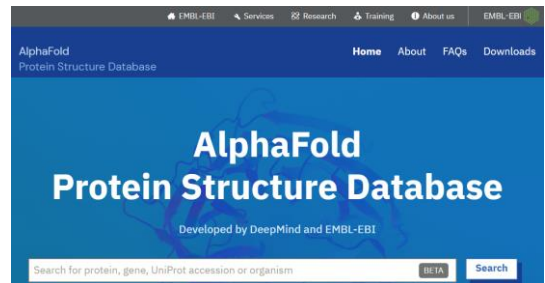
# AlphaFold



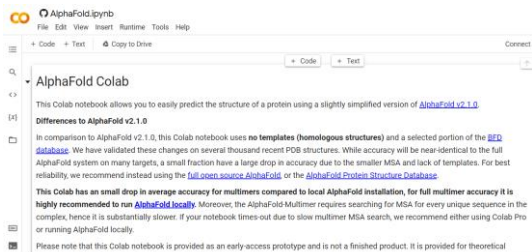
# AlphaFold



# AlphaFold



# AlphaFold



The screenshot shows the top portion of a Google Colab notebook titled "AlphaFold Colab". The interface includes a menu bar with "File", "Edit", "View", "Insert", "Runtime", "Tools", and "Help". Below the menu bar are tabs for "Code" and "Text", and a "Connect" button. The notebook content begins with the title "AlphaFold Colab" and a paragraph explaining that the notebook allows for easy prediction of protein structure using a simplified version of AlphaFold v2.1.0. A section titled "Differences to AlphaFold v2.1.0" follows, detailing that this version lacks templates and uses a smaller MSA database, leading to lower accuracy. It also notes a significant drop in accuracy for multimers and recommends running AlphaFold locally for better performance. A final note states that the notebook is an early-access prototype.

AlphaFold Colab

This Colab notebook allows you to easily predict the structure of a protein using a slightly simplified version of [AlphaFold v2.1.0](#).

**Differences to AlphaFold v2.1.0**

In comparison to AlphaFold v2.1.0, this Colab notebook uses **no templates (homologous structures)** and a selected portion of the [PDB database](#). We have validated these changes on several thousand recent PDB structures. While accuracy will be near-identical to the full AlphaFold system on many targets, a small fraction have a large drop in accuracy due to the smaller MSA and lack of templates. For best reliability, we recommend instead using the [full open-source AlphaFold](#) or the [AlphaFold Protein Structure Database](#).

This Colab has an **small drop in average accuracy for multimers** compared to local AlphaFold installation, for **full multimer accuracy it is highly recommended to run AlphaFold locally**. Moreover, the AlphaFold-Multimer requires searching for MSA for every unique sequence in the complex, hence it is substantially slower. If your notebook times-out due to slow multimer MSA search, we recommend either using Colab Pro or running AlphaFold locally.

Please note that this Colab notebook is provided as an early-access prototype and is not a finished product. It is provided for theoretical